

Mang Shi

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/5341132/mang-shi-publications-by-year.pdf>

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

125 papers	8,473 citations	40 h-index	91 g-index
145 ext. papers	11,044 ext. citations	8.4 avg, IF	6.02 L-index

#	Paper	IF	Citations
125	: a new taxonomical framework for a rapidly expanding order of unusual monjiviricete viruses broadly distributed among arthropod subphyla.. <i>Applied and Environmental Microbiology</i> , 2022 , AEM0195421	4.8	1
124	A time-series meta-transcriptomic analysis reveals the seasonal, host, and gender structure of mosquito viromes.. <i>Virus Evolution</i> , 2022 , 8, veac006	3.7	1
123	Co-infecting pathogens can contribute to inflammatory responses and severe symptoms in COVID-19.. <i>Journal of Thoracic Disease</i> , 2022 , 14, 355-370	2.6	0
122	Total infectome characterization of respiratory infections in pre-COVID-19 Wuhan, China.. <i>PLoS Pathogens</i> , 2022 , 18, e1010259	7.6	2
121	Virome characterization of game animals in China reveals a spectrum of emerging pathogens.. <i>Cell</i> , 2022 ,	56.2	11
120	A total infectome approach to understand the etiology of infectious disease in pigs.. <i>Microbiome</i> , 2022 , 10, 73	16.6	1
119	The adenosine analog prodrug ATV006 is orally bioavailable and has preclinical efficacy against parental SARS-CoV-2 and variants.. <i>Science Translational Medicine</i> , 2022 , eabm7621	17.5	3
118	Two Rhabdoviruses, One Novel, Isolated from <i>Armigeres subalbatus</i> in China. <i>Pathogens</i> , 2022 , 11, 624	4.5	1
117	ICTV Virus Taxonomy Profile: Rhabdoviridae 2022. <i>Journal of General Virology</i> , 2022 , 103,	4.9	8
116	Characterization of the Gut Microbiome and Resistomes of Wild and Zoo-Captive Macaques.. <i>Frontiers in Veterinary Science</i> , 2021 , 8, 778556	3.1	0
115	A Novel Bunyavirus Discovered in Oriental Shrimp ().. <i>Frontiers in Microbiology</i> , 2021 , 12, 751112	5.7	2
114	Feline Calicivirus Virulent Systemic Disease: Clinical Epidemiology, Analysis of Viral Isolates and In Vitro Efficacy of Novel Antivirals in Australian Outbreaks. <i>Viruses</i> , 2021 , 13,	6.2	5
113	RNA virome diversity and infection in individual flies. <i>Journal of General Virology</i> , 2021 , 102,	4.9	2
112	Isolation and Identification of a Novel Phlebovirus, Hedi Virus, from Sandflies Collected in China. <i>Viruses</i> , 2021 , 13,	6.2	1
111	A Convenient and Biosafe Replicon with Accessory Genes of SARS-CoV-2 and Its Potential Application in Antiviral Drug Discovery. <i>Virologica Sinica</i> , 2021 , 36, 913-923	6.4	9
110	Rapid isolation and immune profiling of SARS-CoV-2 specific memory B cell in convalescent COVID-19 patients via LIBRA-seq. <i>Signal Transduction and Targeted Therapy</i> , 2021 , 6, 195	21	10
109	A Novel Virus of Associated with Sexual Precocity in. <i>MSystems</i> , 2021 , 6, e0000321	7.6	3

108	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021 , 166, 3513-3566	2.6	10
107	Association between the nasopharyngeal microbiome and metabolome in patients with COVID-19. <i>Synthetic and Systems Biotechnology</i> , 2021 , 6, 135-143	4.2	9
106	RNA virome abundance and diversity is associated with host age in a bird species. <i>Virology</i> , 2021 , 561, 98-106	3.6	4
105	Virome of bat-infesting arthropods: highly divergent viruses in different vectors. <i>Journal of Virology</i> , 2021 , JVI0146421	6.6	6
104	Use of partial N-gene sequences as a tool to monitor progress on rabies control and elimination efforts in Ethiopia. <i>Acta Tropica</i> , 2021 , 221, 106022	3.2	2
103	Wildlife-borne microorganisms and strategies to prevent and control emerging infectious diseases. <i>Journal of Biosafety and Biosecurity</i> , 2021 , 3, 67-71	1.4	1
102	A comprehensive evolutionary and epidemiological characterization of insertion and deletion mutations in SARS-CoV-2 genomes.. <i>Virus Evolution</i> , 2021 , 7, veab104	3.7	2
101	Meta-Transcriptomic Identification of Divergent in Fish. <i>Viruses</i> , 2020 , 12,	6.2	2
100	Unmapped RNA Virus Diversity in Termites and their Symbionts. <i>Viruses</i> , 2020 , 12,	6.2	4
99	Molecular Epidemiology and Vaccine Compatibility Analysis of Seasonal Influenza Viruses in Wuhan, 2016-2019. <i>Virologica Sinica</i> , 2020 , 35, 556-565	6.4	
98	Insights into the evolutionary history and epidemiological characteristics of the emerging lineage 1 porcine reproductive and respiratory syndrome viruses in China. <i>Transboundary and Emerging Diseases</i> , 2020 , 67, 2630-2641	4.2	9
97	Transcriptomic characteristics of bronchoalveolar lavage fluid and peripheral blood mononuclear cells in COVID-19 patients. <i>Emerging Microbes and Infections</i> , 2020 , 9, 761-770	18.9	671
96	High resolution metagenomic characterization of complex infectomes in paediatric acute respiratory infection. <i>Scientific Reports</i> , 2020 , 10, 3963	4.9	7
95	Abundant and Diverse RNA Viruses in Insects Revealed by RNA-Seq Analysis: Ecological and Evolutionary Implications. <i>MSystems</i> , 2020 , 5,	7.6	21
94	Metatranscriptomic Analysis of Virus Diversity in Urban Wild Birds with Paretic Disease. <i>Journal of Virology</i> , 2020 , 94,	6.6	11
93	Identification of A Novel Papillomavirus Associated with Squamous Cell Carcinoma in A Domestic Cat. <i>Viruses</i> , 2020 , 12,	6.2	6
92	A new lineage of segmented RNA viruses infecting animals. <i>Virus Evolution</i> , 2020 , 6, vez061	3.7	17
91	Clinical and epidemiological features of COVID-19 family clusters in Beijing, China. <i>Journal of Infection</i> , 2020 , 81, e26-e30	18.9	57

90	RNA based mNGS approach identifies a novel human coronavirus from two individual pneumonia cases in 2019 Wuhan outbreak. <i>Emerging Microbes and Infections</i> , 2020 , 9, 313-319	18.9	337
89	Phylogenetics, Genomic Recombination, and NSP2 Polymorphic Patterns of Porcine Reproductive and Respiratory Syndrome Virus in China and the United States in 2014-2018. <i>Journal of Virology</i> , 2020 , 94,	6.6	27
88	Novel hepaci- and pegi-like viruses in native Australian wildlife and non-human primates. <i>Virus Evolution</i> , 2020 , 6, veaa064	3.7	6
87	Risk factors for the critical illness in SARS-CoV-2 infection: a multicenter retrospective cohort study. <i>Respiratory Research</i> , 2020 , 21, 277	7.3	6
86	Emerging Sand Fly-Borne Phlebovirus in China. <i>Emerging Infectious Diseases</i> , 2020 , 26, 2435-2438	10.2	6
85	Enteric involvement in hospitalised patients with COVID-19 outside Wuhan. <i>The Lancet Gastroenterology and Hepatology</i> , 2020 , 5, 534-535	18.8	97
84	Comparative Analysis of RNA Virome Composition in Rabbits and Associated Ectoparasites. <i>Journal of Virology</i> , 2020 , 94,	6.6	15
83	Sustained RNA virome diversity in Antarctic penguins and their ticks. <i>ISME Journal</i> , 2020 , 14, 1768-1782	11.9	28
82	Meta-Transcriptomic Analysis Reveals the Virome and Viral Genomic Evolution of Medically Important Mites. <i>Journal of Virology</i> , 2020 ,	6.6	5
81	Virome heterogeneity and connectivity in waterfowl and shorebird communities. <i>ISME Journal</i> , 2019 , 13, 2603-2616	11.9	36
80	Taxonomy of the order Mononegavirales: update 2019. <i>Archives of Virology</i> , 2019 , 164, 1967-1980	2.6	133
79	The discovery of three new hare lagoviruses reveals unexplored viral diversity in this genus. <i>Virus Evolution</i> , 2019 , 5, vez005	3.7	10
78	Fecal Viral Diversity of Captive and Wild Tasmanian Devils Characterized Using Virion-Enriched Metagenomics and Metatranscriptomics. <i>Journal of Virology</i> , 2019 , 93,	6.6	29
77	Meta-transcriptomics reveals a diverse antibiotic resistance gene pool in avian microbiomes. <i>BMC Biology</i> , 2019 , 17, 31	7.3	40
76	Discovery and Prevalence of Divergent RNA Viruses in European Field Voles and Rabbits. <i>Viruses</i> , 2019 , 12,	6.2	2
75	Tamdy Virus in Ixodid Ticks Infesting Bactrian Camels, Xinjiang, China, 2018. <i>Emerging Infectious Diseases</i> , 2019 , 25, 2136-2138	10.2	9
74	Evolution of Termite Symbiosis Informed by Transcriptome-Based Phylogenies. <i>Current Biology</i> , 2019 , 29, 3728-3734.e4	6.3	50
73	Novel hepatitis D-like agents in vertebrates and invertebrates. <i>Virus Evolution</i> , 2019 , 5, vez021	3.7	34

72	Meta-Transcriptomic Comparison of the RNA Viromes of the Mosquito Vectors and in Northern Europe. <i>Viruses</i> , 2019 , 11,	6.2	33
71	Diversity and Evolution of Novel Invertebrate DNA Viruses Revealed by Meta-Transcriptomics. <i>Viruses</i> , 2019 , 11,	6.2	4
70	Metagenomic discovery and co-infection of diverse wobbly possum disease viruses and a novel hepatitis virus in Australian brushtail possums. <i>One Health Outlook</i> , 2019 , 1, 5	5	9
69	Extensive Diversity of RNA Viruses in Australian Ticks. <i>Journal of Virology</i> , 2019 , 93,	6.6	63
68	Using Metagenomics to Characterize an Expanding Virosphere. <i>Cell</i> , 2018 , 172, 1168-1172	56.2	134
67	The evolutionary history of vertebrate RNA viruses. <i>Nature</i> , 2018 , 556, 197-202	50.4	354
66	Meta-transcriptomics and the evolutionary biology of RNA viruses. <i>Virus Research</i> , 2018 , 243, 83-90	6.4	72
65	No detectable effect of Mel on the prevalence and abundance of the RNA virome of. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018 , 285,	4.4	37
64	A Novel Hepadnavirus Identified in an Immunocompromised Domestic Cat in Australia. <i>Viruses</i> , 2018 , 10,	6.2	19
63	The diversity, evolution and origins of vertebrate RNA viruses. <i>Current Opinion in Virology</i> , 2018 , 31, 9-16	7.5	33
62	Viral Discovery in the Invasive Australian Cane Toad (<i>Rhinella marina</i>) Using Metatranscriptomic and Genomic Approaches. <i>Journal of Virology</i> , 2018 , 92,	6.6	7
61	Complete genome of <i>Aedes aegypti</i> anphevirus in the Aag2 mosquito cell line. <i>Journal of General Virology</i> , 2018 , 99, 832-836	4.9	9
60	Hidden diversity and evolution of viruses in market fish. <i>Virus Evolution</i> , 2018 , 4, vey031	3.7	30
59	A Divergent Hepatitis D-Like Agent in Birds. <i>Viruses</i> , 2018 , 10,	6.2	41
58	Virus-virus interactions and host ecology are associated with RNA virome structure in wild birds. <i>Molecular Ecology</i> , 2018 , 27, 5263-5278	5.7	49
57	Transcriptome Analysis and In Situ Hybridization for FcaGHV1 in Feline Lymphoma. <i>Viruses</i> , 2018 , 10,	6.2	1
56	Surveillance of Bat Coronaviruses in Kenya Identifies Relatives of Human Coronaviruses NL63 and 229E and Their Recombination History. <i>Journal of Virology</i> , 2017 , 91,	6.6	134
55	Diversity, evolution and population dynamics of avian influenza viruses circulating in the live poultry markets in China. <i>Virology</i> , 2017 , 505, 33-41	3.6	19

54	Dinucleotide Composition in Animal RNA Viruses Is Shaped More by Virus Family than by Host Species. <i>Journal of Virology</i> , 2017 , 91,	6.6	57
53	A Diverse Range of Novel RNA Viruses in Geographically Distinct Honey Bee Populations. <i>Journal of Virology</i> , 2017 , 91,	6.6	88
52	The history of rabies in the Western Hemisphere. <i>Antiviral Research</i> , 2017 , 146, 221-232	10.8	49
51	Successful strategies implemented towards the elimination of canine rabies in the Western Hemisphere. <i>Antiviral Research</i> , 2017 , 143, 1-12	10.8	54
50	<i>Francisella tularensis</i> ssp. <i>holarctica</i> in Ringtail Possums, Australia. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1198-1201	10.2	28
49	Characterizing the virome of <i>Ixodes ricinus</i> ticks from northern Europe. <i>Scientific Reports</i> , 2017 , 7, 108704.9	4.9	57
48	Diversity of Middle East respiratory syndrome coronaviruses in 109 dromedary camels based on full-genome sequencing, Abu Dhabi, United Arab Emirates. <i>Emerging Microbes and Infections</i> , 2017 , 6, e101	18.9	26
47	High-Resolution Metatranscriptomics Reveals the Ecological Dynamics of Mosquito-Associated RNA Viruses in Western Australia. <i>Journal of Virology</i> , 2017 , 91,	6.6	104
46	Redefining the invertebrate RNA virosphere. <i>Nature</i> , 2016 , 540, 539-543	50.4	821
45	Divergent Viruses Discovered in Arthropods and Vertebrates Revise the Evolutionary History of the Flaviviridae and Related Viruses. <i>Journal of Virology</i> , 2016 , 90, 659-69	6.6	162
44	Diversity and evolution of avian influenza viruses in live poultry markets, free-range poultry and wild wetland birds in China. <i>Journal of General Virology</i> , 2016 , 97, 844-854	4.9	34
43	Taxonomy of the order Mononegavirales: update 2016. <i>Archives of Virology</i> , 2016 , 161, 2351-60	2.6	324
42	Identification of novel and diverse rotaviruses in rodents and insectivores, and evidence of cross-species transmission into humans. <i>Virology</i> , 2016 , 494, 168-77	3.6	46
41	Fourteen types of co-circulating recombinant enterovirus were associated with hand, foot, and mouth disease in children from Wenzhou, China. <i>Journal of Clinical Virology</i> , 2015 , 70, 29-38	14.5	34
40	Importation and Recombination Are Responsible for the Latest Emergence of Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus in China. <i>Journal of Virology</i> , 2015 , 89, 10712-6	6.6	129
39	Isolation and characterization of a novel arenavirus harbored by Rodents and Shrews in Zhejiang province, China. <i>Virology</i> , 2015 , 476, 37-42	3.6	44
38	Discovery, diversity and evolution of novel coronaviruses sampled from rodents in China. <i>Virology</i> , 2015 , 474, 19-27	3.6	84
37	Other Bat-Borne Viruses 2015 , 217-247		3

36	Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. <i>ELife</i> , 2015 , 4,	8.9	435
35	Genomic characterization of emergent pseudorabies virus in China reveals marked sequence divergence: Evidence for the existence of two major genotypes. <i>Virology</i> , 2015 , 483, 32-43	3.6	70
34	Author response: Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses 2015 ,		4
33	Evolutionary diversification of type 2 porcine reproductive and respiratory syndrome virus. <i>Journal of General Virology</i> , 2015 , 96, 1570-80	4.9	49
32	A tick-borne segmented RNA virus contains genome segments derived from unsegmented viral ancestors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6744-9	11.5	104
31	Second-pandemic strain of <i>Vibrio cholerae</i> from the Philadelphia cholera outbreak of 1849. <i>New England Journal of Medicine</i> , 2014 , 370, 334-40	59.2	104
30	Extensive diversity of Rickettsiales bacteria in two species of ticks from China and the evolution of the Rickettsiales. <i>BMC Evolutionary Biology</i> , 2014 , 14, 167	3	71
29	Genomic evolution of porcine reproductive and respiratory syndrome virus (PRRSV) isolates revealed by deep sequencing. <i>PLoS ONE</i> , 2014 , 9, e88807	3.7	36
28	The spread of type 2 Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in North America: a phylogeographic approach. <i>Virology</i> , 2013 , 447, 146-54	3.6	36
27	Systematic phylogenetic analysis of influenza A virus reveals many novel mosaic genome segments. <i>Infection, Genetics and Evolution</i> , 2013 , 18, 367-78	4.5	18
26	Discovery of diverse polyomaviruses in bats and the evolutionary history of the Polyomaviridae. <i>Journal of General Virology</i> , 2013 , 94, 738-748	4.9	47
25	Evolutionary history and phylogeography of rabies viruses associated with outbreaks in Trinidad. <i>PLoS Neglected Tropical Diseases</i> , 2013 , 7, e2365	4.8	16
24	New world bats harbor diverse influenza A viruses. <i>PLoS Pathogens</i> , 2013 , 9, e1003657	7.6	825
23	Recombination is associated with an outbreak of novel highly pathogenic porcine reproductive and respiratory syndrome viruses in China. <i>Journal of Virology</i> , 2013 , 87, 10904-7	6.6	57
22	Phylodynamics of H5N1 avian influenza virus in Indonesia. <i>Molecular Ecology</i> , 2012 , 21, 3062-77	5.7	28
21	Complete genome characterization of a East European Type 1 subtype 3 porcine reproductive and respiratory syndrome virus. <i>Virus Genes</i> , 2012 , 44, 51-4	2.3	14
20	Genomic characterization of seven distinct bat coronaviruses in Kenya. <i>Virus Research</i> , 2012 , 167, 67-73	6.4	24
19	A distinct lineage of influenza A virus from bats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 4269-74	11.5	741

18	Molecular inferences suggest multiple host shifts of rabies viruses from bats to mesocarnivores in Arizona during 2001-2009. <i>PLoS Pathogens</i> , 2012 , 8, e1002786	7.6	117
17	Evolutionary conservation of the PA-X open reading frame in segment 3 of influenza A virus. <i>Journal of Virology</i> , 2012 , 86, 12411-3	6.6	80
16	Genetic characterization and evolutionary analysis of 4 Newcastle disease virus isolate full genomes from waterbirds in South China during 2003-2007. <i>Veterinary Microbiology</i> , 2011 , 152, 46-54	3.3	26
15	Genetic diversity and multiple introductions of porcine reproductive and respiratory syndrome viruses in Thailand. <i>Virology Journal</i> , 2011 , 8, 164	6.1	12
14	Porcine reproductive and respiratory syndrome virus in Ontario, Canada 1999 to 2010: genetic diversity and restriction fragment length polymorphisms. <i>Journal of General Virology</i> , 2011 , 92, 1391-1397	4.9	16
13	Phylogeny-based evolutionary, demographical, and geographical dissection of North American type 2 porcine reproductive and respiratory syndrome viruses. <i>Journal of Virology</i> , 2010 , 84, 8700-11	6.6	238
12	Molecular epidemiology of PRRSV: a phylogenetic perspective. <i>Virus Research</i> , 2010 , 154, 7-17	6.4	227
11	New rabies virus variant found during an epizootic in white-nosed coatis from the Yucatan Peninsula. <i>Epidemiology and Infection</i> , 2010 , 138, 1586-9	4.3	18
10	Phylogenetic perspectives on the epidemiology and origins of SARS and SARS-like coronaviruses. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 1185-96	4.5	31
9	Phylogenetic evidence for homologous recombination within the family Birnaviridae. <i>Journal of General Virology</i> , 2008 , 89, 3156-3164	4.9	39
8	Meta-transcriptomic analysis of virus diversity in urban wild birds with parietic disease		1
7	The discovery of three new hare lagoviruses reveals unexplored viral diversity in this genus		1
6	A new lineage of segmented RNA viruses infecting animals		1
5	Sustained virome diversity in Antarctic penguins and their ticks: geographical connectedness and no evidence for low pathogen pressure		3
4	Metagenomic identification of diverse animal hepaciviruses and pegiviruses		1
3	Extensive Diversity of RNA Viruses in Australian Ticks		2
2	A divergent hepatitis D-like agent in birds		1
1	Characterisation of the faecal virome of captive and wild Tasmanian devils using virus-like particles metagenomics and meta-transcriptomics		3

